

0272wo310_v2_ST25.txt
SEQUENCE LISTING

<110> Bayer HealthCare LLC
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Andersen, Kim Vilbour
Ropke, Mads
Glazer, Steven

<120> FVII or FVIIa Variants

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<150> US 60/456,547
<151> 2003-03-20

<150> US 60/479,708
<151> 2003-06-19

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<170> PatentIn version 3.5

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Ala		
	1	
aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc		165
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys		
5 10 15		
aaa gag gaa cag tgc agc ttt gag gaa gcc cg 1		213
Lys Glu Glu Gln Cys Ser Phe Glu Ala Arg Glu Ile Phe Lys Asp		
20 25 30		
gct gag cg 261		
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln		
35 40 45		
tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg		309
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu		
50 55 60 65		
cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc		357
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys		
70 75 80		
gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc		405
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly		
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tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro 115 120 125	501
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cg ^g aac Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn 130 135 140 145	549
gct agc aaa ccc cag ggc cg ^g atc gtc ggc ggg aag gtc tgc cct aag Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Lys Val Cys Pro Lys 150 155 160	597
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu 165 170 175	645
tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His 180 185 190	693
tgc ttc gat aag att aag aat tgg cg ^g aac ctc atc gct gtg ctc ggc Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly 195 200 205	741
gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cg ^g gtg Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Arg Val 210 215 220 225	789
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His 230 235 240	837
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His 245 250 255	885
gtc gtg cct ctg tgc ctg cct gag cg ^g acc ttt agc gaa cgc acg ctg Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu 260 265 270	933
gct ttc gtc cg ^g ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp 275 280 285	981
cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cg ^g ctg Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu 290 295 300 305	1029
atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro 310 315 320	1077
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35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
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Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
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Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
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Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
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Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145 150 155 160

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Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
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Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
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Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
260 265 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
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Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
290 295 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305 310 315 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
325 330 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
340 345 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
355 360 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
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gcgcggggcc aatgcctttc tggaagagct ccgcctggc tccctggAAC gcgaatgcaa	180
agaggaacAG tgcagcttg aggaAGCCG ggagatttc aaagacgctg agcggaccAA	240
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cgtgcCTCTG tgcctgcCTG agcggACCTT tagcgaACGC acgCTGGCTT tcgtCCGCTT	960
tagcCTCGTG tccggCTGGG gCCAGCTGCT CGACCggggc gctaccGCTC tcgagCTGAT	1020
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tagCTGCAAG ggggACTCCG CGGGGCCCCA tgccacGcac tATCGCGGGa CCTGGTACCT	1200
caccGGGATC gtcagCTGGG gCCAGGGCTG CGCCACGGTG gggcactttG gcgtctacac	1260
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<220>
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<220>
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<400> 8
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<220>
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